BIOTECHNOLOGY
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P-11-12

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RAW SEQUENCE LISTING
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Application Serial Number: _____09/688,672_____

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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NOV 0 4 2002
TECH CENTER 1600/2900
1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/688,672

DATE: 10/25/2002
TIME: 15:44:11

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

```
  3 <110> APPLICANT: Skeiky, Yasir
  4         Reed, Steven
  5         Houghton, Raymond L.
  6         McNeill, Patricia D.
  7         Dillon, Davin C.
  8         Lodes, Michael L.
  9         Corixa Corporation
 11 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 13 <130> FILE REFERENCE: 014058-009041US
 15 <140> CURRENT APPLICATION NUMBER: US 09/688,672
 16 <141> CURRENT FILING DATE: 2000-10-10
 18 <150> PRIOR APPLICATION NUMBER: US 60/158,338
 19 <151> PRIOR FILING DATE: 1999-10-07
 21 <150> PRIOR APPLICATION NUMBER: US 60/158,425
 22 <151> PRIOR FILING DATE: 1999-10-07
 24 <160> NUMBER OF SEQ ID NOS: 202
 26 <170> SOFTWARE: PatentIn Ver. 2.1
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See also p. 14 for additional errors

ERRORED SEQUENCES

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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1088 <210> SEQ ID NO: 16
1089 <211> LENGTH: 239
1090 <212> TYPE: PRT
1091 <213> ORGANISM: Artificial Sequence
W--> 1092 <220> FEATURE:
1092 <223> OTHER INFORMATION: Description of Artificial Sequence:HTCC#1 (1-232)
E--> 1094 <400> SEQUENCE: 16
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↑ throughout
→ missing <220> (mandatory heading)

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1096  1               5                 10                15
1098 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
1099               20                  25                30
1101 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
1102            35                  40                45
1104 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
1105        50                  55                60
1107 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
1108 65                  70                75                80
1110 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
1111               85                  90                95
1113 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
1114            100                 105               110
1116 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
```

RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:12

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

```
1117        115                120                125
1119 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
1120      130                135           .         140
1122 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
1123 145                150                155                160
1125 Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
1126                165                170                175
1128 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
1129          180                185                190
1131 Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
1132          195                200                205
1134 Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
1135      210                215                220
1137 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
1138 225                230                235
1212 <210> SEQ ID NO: 18
1213 <211> LENGTH: 216
1214 <212> TYPE: PRT
1215 <213> ORGANISM: Artificial Sequence
W--> 1216 <220> FEATURE:
1216 <223> OTHER INFORMATION: Description of Artificial Sequence:HTCC#1
1217      (184-392)
E--> 1219 <400> SEQUENCE: 18
1220 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
1221   1           5                10                15
1223 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
1224                20                25                30
1226 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
1227          35                40                45           .
1229 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
1230      50                55                60
1232 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
1233 65                70                75                80
1235 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
1236            _ 85                90                95
1238 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
1239          100                105                110
1241 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
1242      115                120                125
1244 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
1245      130                135                140
1247 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
1248 145                150                155                160
1250 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
1251                165                170                175
1253 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
1254          180                185                190
1256 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
1257      195                200                205
```

RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:12

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

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     1260     210                 215
     1313 <210> SEQ ID NO: 20
     1314 <211> LENGTH: 136
     1315 <212> TYPE: PRT
     1316 <213> ORGANISM: Artificial Sequence
W--> 1317 <220> FEATURE:
     1317 <223> OTHER INFORMATION: Description of Artificial Sequence:HTCC#1 (1-129)
E--> 1319 <400> SEQUENCE: 20
     1320 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
     1321   1                   5                 10                  15
     1323 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
     1324              20                  25                  30
     1326 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
     1327              35                  40                  45
     1329 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
     1330          50                  55                  60
     1332 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
     1333  65                  70                  75                  80
     1335 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
     1336              85                  90                  95
     1338 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
     1339              100                 105                 110
     1341 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
     1342          115                 120                 125
     1344 Ile Pro Val Val Gly His Ala Leu
     1345      130                 135
     1466 <210> SEQ ID NO: 22
     1467 <211> LENGTH: 403
     1468 <212> TYPE: PRT
     1469 <213> ORGANISM: Artificial Sequence
W--> 1470 <220> FEATURE:
     1470 <223> OTHER INFORMATION: Description of Artificial Sequence:HTCC#1 (TM-1)
E--> 1472 <400> SEQUENCE: 22
     1473 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
     1474   1                   5                 10                  15
     1476 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
     1477              20                  25                  30
     1479 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
     1480              35                  40                  45
     1482 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
     1483          50                  55                  60
     1485 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
     1486  65                  70                  75                  80
     1488 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
     1489              85                  90                  95
     1491 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
     1492              100                 105                 110
     1494 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
```

```
1495         115                  120                  125
1497 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
1498     130                  135                  140
1500 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala Tyr
1501 145                  150                  155              160
1503 Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu Lys
1504             165                  170                  175
1506 Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile
1507         180                  185                  190
1509 Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp
1510         195                  200                  205
1512 Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
1513     210                  215                  220
1515 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
1516 225                  230                  235              240
1518 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
1519             245                  250                  255
1521 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
1522         260                  265                  270
1524 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
1525         275                  280                  285
1527 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
1528     290                  295                  300
1530 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
1531 305                  310                  315              320
1533 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
1534             325                  330                  335
1536 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
1537         340                  345                  350
1539 Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
1540         355                  360                  365
1542 Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
1543     370                  375                  380
1545 Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
1546 385                  390                  395              400
1548 Asn Val Val
1669 <210> SEQ ID NO: 24
1670 <211> LENGTH: 403
1671 <212> TYPE: PRT
1672 <213> ORGANISM: Artificial Sequence
W--> 1673 <220> FEATURE:
1673 <223> OTHER INFORMATION: Description of Artificial Sequence:HTCC#1 (TM-2)
E--> 1675 <400> SEQUENCE: 24
1676 Met His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1677  1               5                  10                  15
1679 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
1680         20                  25                  30
1682 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
1683         35                  40                  45
```

```
1685 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
1686      50              55              60
1688 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
1689 65              70              75              80
1691 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
1692              85              90              95
1694 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu Glu
1695              100             105             110
1697 Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu
1698              115             120             125
1700 Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala
1701      130             135             140
1703 Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr
1704 145             150             155             160
1706 Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu
1707              165             170             175
1709 Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser
1710              180             185             190
1712 Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe
1713              195             200             205
1715 Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
1716      210             215             220
1718 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
1719 225             230             235             240
1721 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
1722              245             250             255
1724 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
1725              260             265             270
1727 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
1728              275             280             285
1730 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
1731      290             295             300
1733 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
1734 305             310             315             320
1736 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
1737              325             330             335
1739 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
1740              340             345             350
1742 Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
1743              355             360             365
1745 Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
1746      370             375             380
1748 Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
1749 385             390             395             400
1751 Asn Val Val
3709 <210> SEQ ID NO: 58
3710 <211> LENGTH: 740
3711 <212> TYPE: PRT
3712 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:13

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

W--> 3713 <220> FEATURE:
     3713 <223> OTHER INFORMATION: Description of Artificial Sequence:fusion protein
     3714   HTCC#1(184-392)-TbH9-HTCC#1(1-129)
E--> 3716 <400> SEQUENCE: 58
     3717 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Thr
     3718 1   5   10   15
     3720 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
     3721   20   25   30
     3723 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
     3724   35   40   45
     3726 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
     3727   50   55   60
     3729 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
     3730 65   70   75   80
     3732 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
     3733   85   90   95
     3735 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
     3736   100   105   110
     3738 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
     3739   115   120   125
     3741 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
     3742   130   135   140
     3744 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
     3745 145   150   155   160
     3747 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
     3748   165   170   175
     3750 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
     3751   180   185   190
     3753 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
     3754   195   200   205
     3756 Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly Ala
     3757   210   215   220
     3759 Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser
     3760 225   230   235   240
     3762 Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp
     3763   245   250   255
     3765 Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr
     3766   260   265   270
     3768 Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala
     3769   275   280   285
     3771 Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu
     3772   290   295   300
     3774 Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr
     3775 305   310   315   320
     3777 Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
     3778   325   330   335
     3780 Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
     3781   340   345   350
     3783 Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala

RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:13

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

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3784            355                 360                 365
3786 Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
3787     370                 375                 380
3789 Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
3790 385                 390                 395                 400
3792 Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
3793                 405                 410                 415
3795 Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
3796             420                 425                 430
3798 Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
3799         435                 440                 445
3801 Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
3802     450                 455                 460
3804 Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
3805 465                 470                 475                 480
3807 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
3808             485                 490                 495
3810 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
3811         500                 505                 510
3813 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
3814         515                 520                 525
3816 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
3817     530                 535                 540
3819 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
3820 545                 550                 555                 560
3822 Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
3823             565                 570                 575
3825 Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
3826         580                 585                 590
3828 Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
3829         595                 600                 605
3831 Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
3832     610                 615                 620
3834 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
3835 625                 630                 635                 640
3837 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
3838             645                 650                 655
3840 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
3841         660                 665                 670
3843 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
3844     675                 680                 685
3846 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
3847     690                 695                 700
3849 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
3850 705                 710                 715                 720
3852 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
3853             725                 730                 735
3855 Gly His Ala Leu
3856             740
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RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:13

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

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        4072 <210> SEQ ID NO: 60
        4073 <211> LENGTH: 783
        4074 <212> TYPE: PRT
        4075 <213> ORGANISM: Artificial Sequence
W--> 4076 <220> FEATURE:
        4076 <223> OTHER INFORMATION: Description of Artificial Sequence:fusion protein
        4077       HTCC#1(1-149)-TbH9-HTCC#1(161-392)
E--> 4079 <400> SEQUENCE: 60
        4080 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
        4081  1               5                   10                  15
        4083 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
        4084              20                  25                  30
        4086 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
        4087          35                  ·40                  45
        4089 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
        4090          50                  55                  60
        4092 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
        4093  65                  70                  75                  80
        4095 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
        4096              85                  90                  95
        4098 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
        4099              100                 105                 110
        4101 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
        4102          115                 120                 125
        4104 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
        4105      130                 135                 140
        4107 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met Val
        4108 145                 150                 155                 160
        4110 Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala
        4111              165                 170                 175
        4113 Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser
        4114              180                 185              190
        4116 Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val
        4117          195                 200                 205
        4119 Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met
        4120      210                 215                 220
        4122 Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly
        4123 225                 230                 235                 240
        4125 Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr
        4126              245                 250                 255
        4128 Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn
        4129              260                 265                 270
        4131 Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn
        4132          275                 280                 285
        4134 Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala
        4135      290                 295                 300
        4137 Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala
        4138 305                 310                 315                 320
        4140 Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala
```

RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:13

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

```
4141                 325              330              335
4143 Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr
4144             340              345              350
4146 Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln
4147         355              360              365
4149 Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly
4150     370              375              380
4152 Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val
4153 385              390              395              400
4155 Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met
4156             405              410              415
4158 Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
4159         420              425              430
4161 Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser
4162         435              440              445
4164 Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala
4165     450              455              460
4167 Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln
4168 465              470              475              480
4170 Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu
4171             485              490              495
4173 Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met
4174         500              505              510
4176 Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly
4177         515              520              525
4179 Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His
4180     530              535              540
4182 Ser Pro Ala Ala Gly Lys Leu Thr Gln Leu Leu Lys Leu Leu Ala Lys
4183 545              550          ,   555              560
4185 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
4186             565              570              575
4188 Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
4189         580              585              590
4191 Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
4192         595              600              605
4194 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe
4195     610              615              620
4197 Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val
4198 625              630              635              640
4200 Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala
4201             645              650              655
4203 His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly
4204         660              665              670
4206 Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val
4207     675              680              685
4209 His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro
4210     690              695              700
4212 Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser
4213 705              710              715              720
```

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

```
4215 Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met
4216             725             730             735
4218 His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser
4219             740             745             750
4221 Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu
4222         755             760             765
4224 Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
4225     770             775             780
4447 <210> SEQ ID NO: 62
4448 <211> LENGTH: 811
4449 <212> TYPE: PRT
4450 <213> ORGANISM: Artificial Sequence
W--> 4451 <220> FEATURE:
4451 <223> OTHER INFORMATION: Description of Artificial Sequence:fusion protein
4452       HTCC#1(184-392)-TbH9-HTCC#1(1-200)
E--> 4454 <400> SEQUENCE: 62
4455 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
4456   1           5               10              15
4458 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
4459             20              25              30
4461 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
4462         35              40              45
4464 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
4465     50              55              60
4467 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
4468 65              70              75              80
4470 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
4471             85              90              95
4473 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
4474             100             105             110
4476 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
4477         115             120             125
4479 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
4480     130             135             140
4482 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
4483 145             150             155             160
4485 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
4486             165             170             175
4488 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
4489         180             185             190
4491 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
4492         195             200             205
4494 Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly Ala
4495     210             215             220
4497 Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser
4498 225             230             235             240
4500 Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp
4501             245             250             255
4503 Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr
```

```
4504                 260                 265                 270
4506 Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala
4507          275                 280                 285
4509 Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu
4510      290                 295                 300
4512 Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr
4513 305                 310                 315                 320
4515 Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
4516              325                 330                 335
4518 Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
4519          340                 345                 350
4521 Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala
4522          355                 360                 365
4524 Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
4525      370                 375                 380
4527 Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
4528 385                 390                 395                 400
4530 Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
4531              405                 410                 415
4533 Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
4534          420                 425                 430
4536 Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
4537          435                 440                 445
4539 Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
4540      450                 455                 460
4542 Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
4543 465                 470                 475                 480
4545 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
4546              485                 490                 495
4548 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
4549          500                 505                 510
4551 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
4552          515                 520                 525
4554 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
4555      530                 535                 540
4557 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
4558 545                 550                 555                 560
4560 Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
4561          565                 570                 575
4563 Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
4564          580                 585                 590
4566 Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
4567      595                 600                 605
4569 Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
4570      610                 615                 620
4572 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
4573 625                 630                 635                 640
4575 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
4576              645                 650                 655
```

```
4578 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
4579             660             665             670
4581 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
4582         675             680             685
4584 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
4585     690             695             700
4587 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
4588 705             710             715             720
4590 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
4591             725             730             735
4593 Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
4594             740             745             750
4596 Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
4597         755             760             765
4599 Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
4600     770             775             780
4602 Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
4603 785             790             795             800
4605 Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile
4606             805             810
4760 <210> SEQ ID NO: 64
4761 <211> LENGTH: 539
4762 <212> TYPE: PRT
4763 <213> ORGANISM: Artificial Sequence
W-->4764 <220> FEATURE:
4764 <223> OTHER INFORMATION: Description of Artificial Sequence:fusion protein
4765        TbRa12-HTCC#1
E-->4767 <400> SEQUENCE: 64
4768 Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
4769   1             5             10             15
4771 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
4772         20             25             30
4774 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
4775     35             40             45
4777 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
4778     50             55             60
4780 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
4781 65             70             75             80
4783 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
4784             85             90             95
4786 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
4787         100             105             110
4789 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
4790     115             120             125
4792 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val Pro
4793     130             135             140
4795 Arg Gly Ser Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
4796 145             150             155             160
4798 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
```

```
4799                 165                170                175
4801 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
4802                 180                185                190
4804 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
4805             195                200                205
4807 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
4808     210                215                220
4810 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
4811 225                230                235                240
4813 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
4814             245                250                255
4816 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
4817             260                265                270
4819 Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
4820         275                280                285
4822 Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
4823     290                295                300
4825 Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
4826 305                310                315                320
4828 Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
4829             325                330                335
4831 Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn
4832             340                345                350
4834 Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu
4835         355                360                365
4837 Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro
4838     370                375                380
4840 Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe
4841 385                390                395                400
4843 Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser
4844             405                410                415
4846 Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly
4847         420                425                430
4849 Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser
4850         435                440                445
4852 Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala
4853     450                455                460
4855 Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser
4856 465                470                475                480
4858 Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser
4859             485                490                495
4861 Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala
4862         500                505                510
4864 Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly
4865         515                520                525
4867 Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
4868     530                535
```

VARIABLE LOCATION SUMMARY   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   TIME: 15:44:15

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:5; N Pos. 406
Seq#:11; N Pos. 325,328,348,353,442,659,679
Seq#:12; Xaa Pos. 63,121,285
Seq#:29; N Pos. 1460,1854
Seq#:33; N Pos. 497,500,1136,1445,1487,1509,1515
Seq#:155; N Pos. 104

VERIFICATION SUMMARY   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672 TIME: 15:44:15

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

```
L:599  M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:599  M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:599  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:360
L:821  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:300
L:823  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:420
L:826  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:600
L:827  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:660
L:853  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48
L:865  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:112
L:895  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:272
L:1083 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:1092 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1094 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:1216 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1219 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:1317 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1319 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:20
L:1470 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:1472 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:1673 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1675 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:24
L:1990 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:29
L:1990 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:29
L:1990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:1440
L:1996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:1800
L:2228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:480
L:2238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:1080
L:2244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:1440
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:1500
L:2481 M:283 W: Missing Blank Line separator, <400> field identifier
L:2482 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (41) SEQUENCE:
L:2486 M:283 W: Missing Blank Line separator, <400> field identifier
L:2487 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (42) SEQUENCE:
L:3497 M:283 W: Missing Blank Line separator, <400> field identifier
L:3498 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (55) SEQUENCE:
L:3502 M:283 W: Missing Blank Line separator, <400> field identifier
L:3503 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:
L:3713 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
L:3716 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:58
L:4076 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:60
L:4079 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:60
L:4451 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:62
L:4454 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:62
L:4757 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:63
L:4764 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:64
L:4767 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:64
L:4872 M:283 W: Missing Blank Line separator, <400> field identifier
L:4873 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (65) SEQUENCE:
```

VERIFICATION SUMMARY   DATE: 10/25/2002
PATENT APPLICATION: US/09/688,672   · TIME: 15:44:15

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\l0242002\I688672.raw

```
L:4877 M:283 W: Missing Blank Line separator, <400> field identifier
L:4878 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:
L:4882 M:283 W: Missing Blank Line separator, <400> field identifier
L:4883 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:
L:4887 M:283 W: Missing Blank Line separator, <400> field identifier
L:4888 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:
L:4892 M:283 W: Missing Blank Line separator, <400> field identifier
L:4893 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:
L:4897 M:283 W: Missing Blank Line separator, <400> field identifier
L:4898 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:
L:4902 M:283 W: Missing Blank Line separator, <400> field identifier
L:4903 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (71) SEQUENCE:
L:4907 M:283 W: Missing Blank Line separator, <400> field identifier
L:4908 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (72) SEQUENCE:
L:4912 M:283 W: Missing Blank Line separator, <400> field identifier
L:4913 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (73) SEQUENCE:
L:4917 M:283 W: Missing Blank Line separator, <400> field identifier
L:4918 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (74) SEQUENCE:
L:4922 M:283 W: Missing Blank Line separator, <400> field identifier
L:4923 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (75) SEQUENCE:
L:4927 M:283 W: Missing Blank Line separator, <400> field identifier
L:4928 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:
L:4932 M:283 W: Missing Blank Line separator, <400> field identifier
L:4933 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (77) SEQUENCE:
L:4937 M:283 W: Missing Blank Line separator, <400> field identifier
L:4938 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (78) SEQUENCE:
L:4942 M:283 W: Missing Blank Line separator, <400> field identifier
L:4943 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:4947 M:283 W: Missing Blank Line separator, <400> field identifier
L:4948 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE:
L:4952 M:283 W: Missing Blank Line separator, <400> field identifier
L:4953 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (81) SEQUENCE:
L:4957 M:283 W: Missing Blank Line separator, <400> field identifier
L:4958 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (82) SEQUENCE:
L:4962 M:283 W: Missing Blank Line separator, <400> field identifier
L:4963 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (83) SEQUENCE:
L:4967 M:283 W: Missing Blank Line separator, <400> field identifier
L:4968 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (84) SEQUENCE:
L:4972 M:283 W: Missing Blank Line separator, <400> field identifier
L:4973 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (85) SEQUENCE:
L:4977 M:283 W: Missing Blank Line separator, <400> field identifier
L:4978 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (86) SEQUENCE:
L:4982 M:283 W: Missing Blank Line separator, <400> field identifier
L:4983 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (87) SEQUENCE:
L:4987 M:283 W: Missing Blank Line separator, <400> field identifier
L:4988 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (88) SEQUENCE:
L:4992 M:283 W: Missing Blank Line separator, <400> field identifier
L:4993 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (89) SEQUENCE:
L:4997 M:283 W: Missing Blank Line separator, <400> field identifier
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/688,672

DATE: 10/25/2002
TIME: 15:44:15

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\10242002\I688672.raw

L:4998 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (90) SEQUENCE:
L:6288 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:155
L:6288 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:155
L:6288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:155 after pos.:60